

Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1238 Std Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 64 .

```

IGIN          Score 15; DB 14; Length 173;
Query Match 100.0%; Pred. No. 1.9e+02;
Best Local Similarity 100.0%; Mismatches 0;
Matches 15; Conservative 0; Indels 0; Gaps 0;
1 TCCATGGTGTCACT 15
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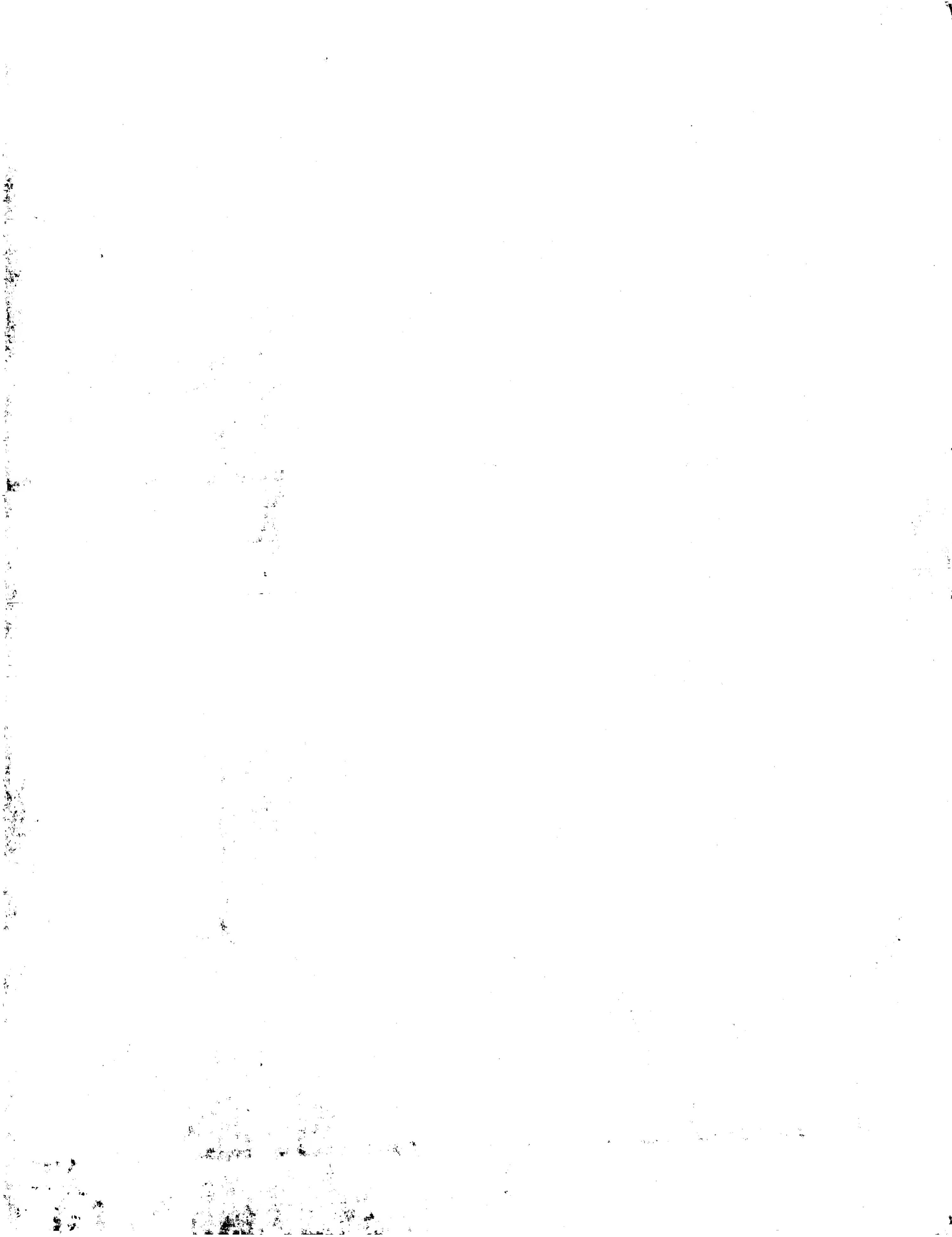
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EST 26-APR-2001
mRNA linear
Xenopus egg library Xenopus
232 bp mRNA linear EST 26-APR-2001
normalized normalized
AW637280 Blackshear/Soares
b156q11:w1 Blackshear/Soares
- 232 bp mRNA linear EST 26-APR-2001
N

Xenopus laevis cDNA clone PBX0056G11 5', mRNA sequence.
AW637280
AW637280.1 GI:7394388
EST.
Xenopus laevis (African clawed frog)
Xenopus laevis
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Mesobatrachia; Pipoidea; Pipidae;
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.

Xenopus,
1 (bases 1 to 232)
Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G.
Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman
, J.W., Bonaldo, M.F. and Soares, M.B.
The NIEHS *Xenopus* maternal EST project: interim analysis of the
first 13,879 ESTs from unfertilized eggs
Gene 267 (1), 71-87 (2001)

GENC 201 (2-7)
21211403
11311557
Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,



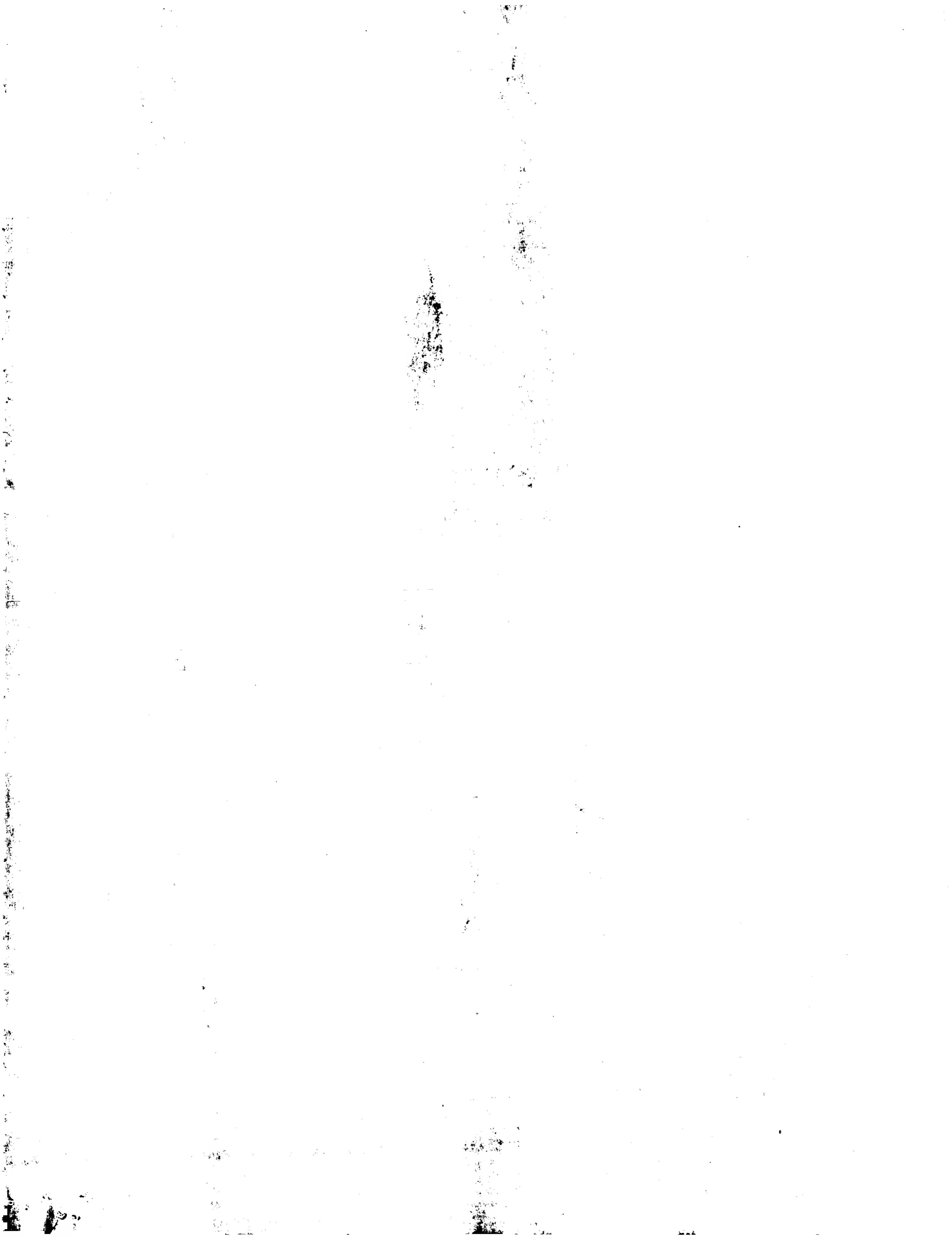
M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)

JOURNAL MEDLINE
PUBMED
COMMENT
TITLE
FEATURES source
LOCUS db43j01.Y1
DEFINITION db43j01.Y1 Blackshear/Soares normalized Xenopus laevis mRNA sequence.
ACCESSION BE132222
VERSION BE132222.1
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.
REFERENCE Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Xenopus EST Project, 1999
JOURNAL Unpublished
COMMENT Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bento Soares and M. Fatima Bonaldo (University of Iowa). DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: infoimage.llnl.gov

Seq Primer: -40RP from Gibco
High quality sequence stop: 268.
Location/Qualifiers
1. 269
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:3301296"
/sex="female"
/tissue_type="unfertilized egg"
/cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DHL0B"
/clone_lib="Blackshear/Soares normalized-Xenopus egg library"
/note="Vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dR18 primer; double stranded cDNAs were ligated to EcoRI adaptors, digested with NotI, and directionally cloned into the NotI and EcoRI-digested pT7T3-Pac vector. The library contained approximately 7.2 x 10^5 recombinants, with average insert sizes of 1-1.5 kb."
BASE COUNT ORIGIN
67 a 46 c 77 g 76 t 2 others
Query Match 100.0%; Score 15; DB 9; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCATGGTGCCTCACT 15
||||||||||||||||
Db 248 TCCATGGTGCCTCACT 262

RESULT 4
BE132222
LOCUS BE132222
DEFINITION 269 bp mRNA linear EST 29-JUN-2000
ACCESSION db43j01.Y1
VERSION BE132222.1
KEYWORDS EST.
SOURCE Xenopus laevis
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus.
REFERENCE Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Xenopus EST Project, 1999
JOURNAL Unpublished
COMMENT Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Bento Soares and M. Fatima Bonaldo (University of Iowa). DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: infoimage.llnl.gov

RESULT 5
BF822715
LOCUS CM3-RT0006-091200-545-c12 RT0006
DEFINITION Homo sapiens cDNA, mRNA sequence.
ACCESSION BF822715
VERSION BF822715.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 321)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
PROC. NATL. ACAD. SCI. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL MEDLINE
COMMENT 20202663
Ludwig Institute for Cancer Research
10737800
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-RT0006-



GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2003, 10:13:13 ; Search time 2294 seconds
 (without alignments)
 158.922 Million cell updates/sec

Title: US-09-716-320-3

Perfect score: 15
 Sequence: 1 tcctatggtgtactca 15

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size : 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:
 1: em_estba:
 2: em_estham:
 3: em_estin:
 4: em_estmu:
 5: em_estov:
 6: em_estpl:
 7: em_estro:
 8: em_htc:
 9: gb_est1:
 10: gb_est2:
 11: gb_htc:
 12: gb_est3:
 13: gb_est4:
 14: gb_est5:
 15: em_estfun:
 16: em_estom:
 17: em_gss_hum:
 18: em_gss_inv:
 19: em_gss_pln:
 20: em_gss_vrt:
 21: em_gss_fun:
 22: em_gss_mam:
 23: em_gss_mus:
 24: em_gss_pro:
 25: em_gss_rod:
 26: em_gss_phg:
 27: em_gss_vrl:
 28: gb_gss1:
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 508: em_gss_vrl:
 509: em_gss_vrl:
 510: em_gss_vrl:
 511: em_gss_vrl:
 512: em

Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 1238 Std Error: 0.00
 Seq primer: mob.REGA+ET
 High quality sequence stop: 64 .
 FEATURES
 Location/Qualifiers
 1. :173
 source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:1253939"
 /db_xref="taxon:9606"
 /clone="IMAGE:310525"
 /tissue_type="senescent fibroblast"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares_senescent_fibroblasts_NbHSF"
 /note="vector: pT7T3D (Pharmacia) with a modified
 polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
 I; 1st strand cDNA was primed with a Not I - oligo(dT)
 primer [5'
 TGTACCAATCTGAAGTGGAGGCCGCATTTTTTTTTTTTT
] double-stranded cDNA was size selected, ligated to Eco
 adapters (Pharmacia), digested with Not I and cloned in
 the Not I and Eco RI sites of a modified pT7T3 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by Ben
 Soares and M.Fatima Bonaldo."
 43 a 33 c 48 g 49 t
 BASE COUNT
 ORIGIN

```

Query Match      100.0%;  Score 15;  DB 14;  Length 173;
Best Local Similarity 100.0%;  Pred. No. 1.9e+02;
Matches 15;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

2Y          1 TCCATGGTCACT 15
            ||||| ||||| |||||
93         93 TCCATGGTCACT 107

```

RESULT	2			
LOCUS	AW637280	232 bp	mRNA	linear
DEFINITION	b156g11.w1 Blackshear/Soares normalized Xenopus laevis cDNA clone PBX0056G11 5'			EST 26-APR-2001
ACCESSION	AW637280			
VERSION	AW637280.1			
KEYWORDS				
SOURCE	Xenopus laevis (African clawed frog)			
ORGANISM	Xenopus laevis			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.			

REFERENCE
AUTHORS Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staffa, N.G.
Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Touchman
'J.W., Bonaldo, M.F. and Soares, M.B.
TITLE The NIEHS Xenopus maternal EST project: interim analysis of the
first 13,879 ESTs from unfertilized eggs
JOURNAL Gene 267 (1), 71-87 (2001)
MEDLINE 21211403
PUBMED 111311557
COMMENT Contact: Perry J. Blackshear
Office of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
USA
Tel: 919 541-4899
Fax: 919 541-4571
Email: black009@niehs.nih.gov
Clone is available through Research Genetics, Inc., 2130 Memorial
Parkway, Huntsville, AL 35901
Phone 800-533-4363 ext.cDNA, fax 256-536-9016 att:cDNA, email

cdna@resgen.com
 DNA Sequencing and analyses performed by National Institutes of
 Health Intramural Sequencing Center (NISC).
 PCR PRimers
 FORWARD: TGTAAACGACGCCAGT
 BACKWARD: CAGGAAACAGCTATGACC
 Plate: 0056 row: G column: 11
 Seq primer: T7 primer.
 FEATURES
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 Location/Qualifiers
 1. .232
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="taxon:8355"
 /clone="PBX0056G11"
 /sex="female"
 /tissue_type="unfertilized egg"
 /cell_type="unfertilized egg"
 /dev_stage="unfertilized egg"
 /lab_host="DH10B"
 /clone_lib="Blackshear/Soares normalized Xenopus egg
 library"
 /note="vector: pT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
 PolyA-selected mRNA was prepared from unfertilized Xenopus
 laevis eggs. The library was constructed in the vector
 pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
 Soares, M.B. 'Normalization and subtraction: two
 approaches to facilitate gene discovery', Genome Research
 6:791-806, 1996. The first strand synthesis used a
 NotI-dT18 primer; double stranded cDNAs were ligated to
 EcoRI adapters, digested with NotI, and directionally
 cloned into the NotI and EcoRI-digested pT7T3-Pac vector.
 The library contained approximately 7.2 x 10^5 recombinants,
 with average insert sizes of 1-1.5 kb." 71 a
 BASE COUNT
 47 t
 49 c
 65 g
 47 a

Query Match	100.0%	Score	15;	DB	9;	Length	232;
Best Local Similarity	100.0%	Pred. NO.	2.1e+02;				
Matches	15;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1 TCCATGGTGGCTCACT	15					
Db	67 TCCATGGTGGCTCACT	81					
RESULT	3						
AA360512	AA360512	268 bp	mRNA	linear	EST	21-APR-1997	
LOCUS	AA360512	T-cell lymphoma	Homo sapiens	CDNA 5'	end similar to		
DEFINITION	EST69742	hereditary multiple exostoses	gene 2 (EXT2),	mRNA sequence.			
ACCESSION	AA360512						
VERSION	AA360512.1	GI:2012902					
KEYWORDS	EST.						
SOURCE	Homo sapiens	(human)					
ORGANISM	Homo sapiens						
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
	1 (bases 1 to 268)						
	Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult						
	, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White						
	, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,						
	Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald						
	, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodek, A.,						
	Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr., Kelley, J.M.,						
	Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelliigrino, S.M.,						
	Phillips, C.A., Ryder, S.E., Scott, J.L., Szaudek, D.M., Utterback, T.R., Weidman, J.F., Shirley, R.,						
	Small, K.V., Spriggs, T.A., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Bednariuk, D.P., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W.,						
	Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon						

M.R., Rosen, C.A., Hasseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.
 Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl.), 3-174 (1995)

JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Other_ESTs: THC194116
 Contact: Kerlavage, AR
 Email: arkerlav@tigr.org
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423

Bioinformatics
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /cell_type="T-lymphocyte"
 /clone_lib="T-cell lymphoma"
 /note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 xhoI"

For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi.html>)

Seq primer: M13 Reverse.

FEATURES
 source
 1. 268
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):164695"
 /cell_type="unfertilized egg"
 /dev_stage="unfertilized egg"
 /lab_host="DH10B"
 /clone_lib="Blackshear/Soares normalized Xenopus egg library"
 /note="Vector: PT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
 PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector PT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B., 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNAs were ligated to EcoRI adaptors, digested with NotI, and directionally cloned into the NotI and EcoRI-digested PT7T3-Pac vector. The library contained approximately 7.2 X 10^5 recombinants, with average insert sizes of 1-1.5 kb."
 BASE COUNT
 ORIGIN
 67 a 46 c 77 g 76 t 2 others

Query Match 100.0%; Score 15; DB 9; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCATGGTGCTCACT 15
 ||||| | | | | | | | |
 Db 248 TCCATGGTGCTCACT 262

RESULT 4
 BE132222
 LOCUS db43901.Y1
 DEFINITION Blackshear/Soares normalized xenopus egg library Xenopus laevis cDNA clone IMAGE:3301296 5', mRNA sequence.

ACCESSION BE132222
 VERSION BE132222.1
 KEYWORDS EST.

SOURCE Xenopus laevis (African clawed frog)
 ORGANISM Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

REFERENCE Clifton, S., Johnson, S.L., Blumberg, B., Song, J., Hillier, L., Pape, D., Martin, J., Wyllie, T., Underwood, K., Theisinger, B., Bowers, Y., Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.

TITLE WashU Xenopus EST project, 1999
 JOURNAL Unpublished
 COMMENT Contact: Sandy Clifton, Ph.D.
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library constructed by Bento Soares and M. Fatima Bonaldo (University of Iowa). DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

Seq primer: -4ORP from Gibco
 High quality sequence stop: 268.
 Location/Qualifiers
 1. 269
 /organism="Xenopus laevis"
 /mol_type="mRNA"
 /db_xref="IMAGE:3301296"
 /sex="female"
 /tissue_type="unfertilized egg"
 /cell_type="unfertilized egg"
 /dev_stage="unfertilized egg"
 /lab_host="DH10B"
 /clone_lib="Blackshear/Soares normalized Xenopus egg library"
 /note="Vector: PT7T3-Pac; Site_1: EcoRI; Site_2: NotI;
 PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector PT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B., 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded cDNAs were ligated to EcoRI adaptors, digested with NotI, and directionally cloned into the NotI and EcoRI-digested PT7T3-Pac vector. The library contained approximately 7.2 X 10^5 recombinants, with average insert sizes of 1-1.5 kb."
 BASE COUNT
 ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 269;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCATGGTGCTCACT 15
 ||||| | | | | | | | |
 Db 196 TCCATGGTGCTCACT. 210

RESULT 5
 BF822715
 LOCUS BF822715
 DEFINITION CM3-RT0006-091200-545-c12 RT0006 HOMO sapiens CDNA, mRNA sequence.
 ACCESSION BF822715
 VERSION BF822715.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 321)
 AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bafia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-RT0006->

091200-545-c12&t3=2000-12-09&t4=1)
Seq primer: puc_18 forward
High quality sequence start: 3
High quality sequence stop: 321.
Location/Qualifiers

1. .321

FEATURES source

1. .321

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="RT0006"
/note="Organ: kidney_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the PUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 88 a 63 c 88 g 82 t

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 321;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 110 TCCATGGTGCTCACT 124

RESULT 6

A1008593/c LOCUS AI008593

DEFINITION EST203044 Normalized rat embryo, Bento Soares Rattus sp. CDNA clone

ACCESSION REMA248

VERSION 3' end, mRNA sequence.

SOURCE EST.

ORGANISM Rattus sp.

REFERENCE Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J., Kerlavage,A.R. and Adams,M.D.

AUTHORS

TITLE Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index

JOURNAL Unpublished

COMMENT Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: rhlee@tigr.org

Seq primer: M13-21.

FEATURES source

1. .322

/organism="Rattus sp."
/mol_type="mRNA"
/db_xref="ATCC (inhost):2016778"
/clone="REMA248"
/dev_stage="embryo 8, 12, 18 dpc"
/clone_lib="Normalized rat embryo, Bento Soares"
/note="Vector: PT7T3Pac; Site_1: ECORI; Site_2: NotI"

BASE COUNT 63 a 94 c 101 g 64 t

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 322;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 285 TCCATGGTGCTCACT 299

RESULT 8

BY400016/c LOCUS BY400016

DEFINITION BY400016 RIKEN full-length enriched, CRL-1722 L5178Y-R Mus musculus

Query Match 100.0%; Score 15; DB 12; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 321 TCCATGGTGCTCACT 307

RESULT 7

B1042474 LOCUS B1042474

DEFINITION RC5-OT0098-220101-011-C05

ACCESSION B1042474

VERSION B1042474.1 GI:14449100

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 329)

AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
Ludwig Institute for Cancer Genetics
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC5&t2=RC5-OT0098-220101-011-C05&t3=2001-01-22&t4=1>)

Seq Primer: puc 18 forward
High quality sequence start: 82
High quality sequence stop: 327.

FEATURES source

1. .329

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="OT0098"
/note="Organ: ovary; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 87 a 59 c 93 g 89 t 1 others

ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 329;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 TCCATGGTGCTCACT 15

Db 285 TCCATGGTGCTCACT 299

FEATURES	Location/Qualifiers
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SOURCE	/organism="Mus musculus"
ORGANISM	/mol_type="mRNA"
KEYWORDS	/strain="DBA/2"
EST.	/db_xref="Taxon:10090"
CDNA clone	/clone="I730028H04"
EST.	/cell_line="CRL-1722 L5178Y-R"
SOURCE	/clone_lib="RIKEN full-length enriched, CRL-1722 L5178Y-R"
ORGANISM	BASE COUNT 106 a 79 c 80 g 91 t 1 others
REFERENCE	Query Match 100.0%; Score 15; DB 13; Length 357;
AUTHORS	Best Local Similarity 100.0%; Pred. No. 2.4e+02;
TITLE	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
JOURNAL	
PUBMED	
COMMENT	
FEATURES	
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KEYWORDS	
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ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGGTCACT 15
 6 TCCATGGTGGTCACT 20

Db

RESULT 10
BG121876

LOCUS 602351302F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4445904 5', mRNA sequence.

ACCESSION BG121876

VERSION BG121876.1 GI:12615385

KEYWORDS EST.

ORGANISM Homo sapiens (human)

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 389)

REFERENCE Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE 20202663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6&t2=RC1-OT0083-120400-h11&t3=2000-04-12&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence stop: 389.

FEATURES

SOURCE

1. 389
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="OT0083"
 /note="Organ: ovary; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 104 a 75 c 104 g 106 t

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 389;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCATGGTGGTCACT 15
 121 TCCATGGTGGTCACT 135

Db

RESULT 12
BIO57614/c

LOCUS BI057614

DEFINITION MR0-GN0175-090301-203-h02 GN0175 Homo sapiens cDNA, mRNA sequence.

ACCESSION BIO57614

VERSION EST.

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 393)

REFERENCE Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE
 20202663
 PUBMED
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-GN0175-090301-203-h02&t3=2001-03-09&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 10
 High quality sequence stop: 364.
 Location/Qualifiers
 1. .393
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="GN0175"
 /note="Organ: Placenta_normal; Vector: puc18; Site_1: Smal ; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
 FEATURES
 source
 BASE COUNT
 ORIGIN
 Query Match 100.0%; Score 15; DB 12; Length 393;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCATGGTGGCTCACT 15
 Db 81 TCCATGGTGGCTCACT 67

RESULT 13
 BH096821/C
 LOCUS BH096821
 DEFINITION RPCI-24-298D11.TJ RPCI-24 Mus musculus genomic clone RPCI-24-298D11
 , genomic survey sequence.
 BH096821.1 GI:14918167
 VERSION BH096821.1
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregiorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Other_GSSS: RPCI-24-298D11.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong

sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE
 20202663
 PUBMED
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (<http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0&t2=MR0-GN0175-090301-203-h02&t3=2001-03-09&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 10
 High quality sequence stop: 364.
 Location/Qualifiers
 1. .393
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-24-298D11"
 /sex="Male"
 /cell_type="Spleen/Brain"
 /clone_lib="RPCI-24"
 /note="Vector: PTARBAC1; Site_1: BamH1; Site_2: BamH1; RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the PTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male C57BL/6J DNA."
 FEATURES
 source
 BASE COUNT
 ORIGIN
 Query Match 100.0%; Score 15; DB 28; Length 398;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TCCATGGTGGCTCACT 15
 Db 250 TCCATGGTGGCTCACT 236

RESULT 14
 AQ296272
 LOCUS AQ296272
 DEFINITION HS_2166_B2_MR_D05 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=10 Row=H, genomic survey sequence.
 ACCESSION AQ296272
 VERSION AQ296272.1 GI:4010340
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Euksaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 400)
 AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 MEDLINE 99380589
 PUBLMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@washington.edu
 Sequence Tagged Connector
 Plate: 2166 row: H column: 10
 Class: BAC ends
 High quality sequence stop: 400.
 Location/Qualifiers
 1. .400
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=2166 Col=10 Row=H"
 /sex="male"

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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ; sperm; Vector: pBelOAC11; BAC Clones in
E-Coli DH10B"
BASE COUNT 99 a 95 c 95 g 111 t
ORIGIN

Query Match 100.0%; Score 15; DB 28; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;
QY 1 TCCATGGTCACT 15
Db 254 TCCATGGTCACT 268

Search completed: September 11, 2003, 11:30:01
Job time : 2295 secs

RESULT 15
R32275
LOCUS R32275 .432 bp mRNA linear EST 28-APR-1995
DEFINITION Yh68e03_r1 Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:134908 , mRNA sequence.
VERSION R32275.1 GI:788118
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; HOMO.
REFERENCE 1 (bases 1 to 432)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1377
High quality sequence stops: 383
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1377 Std Error: 0.00
Seq Primer: M13RP1
High quality sequence stop: 383 .
FEATURES
source
1. .432
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:540785"
/db_xref="taxon:9606"
/clone="IMAGE:134908"
/sex="Female"
/dev_stage="placenta obtained at birth (full term)"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares placenta Nb2HP"
/note="Organ: placenta; Vector: PT7T3D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with Not I - Oligo(dT) primer [5'
AACTGGAAATTCCGGGCCAGGAATTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified PT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
2 others
BASE COUNT 118 a 84 c 110 g 118 t
ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

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